Reference molecule: Cslseq   206 - 2603   (2398 bps)   Homology

Sequence 2: Kukkaseq   48 - 2445   (2398 bps)   94%
Sequence 3: Ds4seq   2 - 2399   (2398 bps)   94%
Sequence 4: 2301SEQ   1 - 2398   (2398 bps)   94%
Sequence 5: 390seq   3 - 2181   (2179 bps)   85%
Sequence 6: H. felis comp 43 - 2475   (2433 bps)   67%
Sequence 7: H. pylori con 2659 - 5088 (2430 bps)   67%
Sequence 8: H. heilmannii 211 - 2636 (2426 bps)   68%

Alignment type: Global DNA
Parameters: Mismatch 1; Open Gap 3; Extend Gap 3

Figure 1a (1)

```
Cslseq       (  686) aaagcctatggcaaacgcctagatattccctcgccaacacgctacggtgggggcaggaagtgcagtttgattcctcttggtgtggcagtaaaaaaagtcgattggcatgaac
Kukkaseq     (  528) .................................................................................a.......................c......
Ds4seq       (  482) ...........................................................................................a...c.........c......
2301SEQ      (  481) ................................................................................................c.......c......
390seq       (  483) ......................t.t...................g.a....a.cag..g.g...t...aac..c..gg..ggaaaaa.gt...g.ac.c....c....t..t..t
H. felis com (  520) ...ag..t.t................t......c....g.a...a.c.t..g..a.c.t.cg..gaaaatcc..ag.a......c....t.ac.g..g.a.ct...at.t..
H. pylori co ( 3136) .a.t.tc..t.......t.......c......g.gagc..g.cag..g..a.at...gaca....gaca..cc..g.ac.c..cgaca.c........a....cgca.tta..tt.c.
H. heilmanni (  691) ...........................................................g.t............c.g.tg.g...t...gg..gaaaaa.cc........

Cslseq       (  806) gggcttgtgaataacatcgcggatga-----------------------------acgccataaactaaagcgcttgacaagcgaaatctcacggattt-------------
Kukkaseq     (  648) ..................................................................................c.......a........a........a...
Ds4seq       (  602) ..............................................................................c............t.a.a..a..
2301SEQ      (  601) ..........................................................................t.t...c........................c......
390seq       (  603) tctt..g...g..cg.caa..c..c------cgatgg...a.actc.gct.aa.acgc..t...gaaa.a..t...gggtctgtaaactgcggttgta-
H. felis com (  640) cat.g..tg...g.cg.caa..a..ca.------cgaaagc...a.a.tt.tt.ac..ga..t...gag.gt..t...catggcgctaaaagcgatgacaac
H. pylori co ( 3256) tatgtaaa.a..t.......taag------------------aa.........a--................t.cg-----
H. heilmanni (  811) .ct..a..cg.caa..c...c.cgatggcaaaaaactcgcccttaaa...gc...g.a..g..ctatc..c.gcggtt.cgac---

Cslseq       (  878) ------------atcaagtaaggagactc------------ccatgaaaatgaaaaa---------------ac----aagaatatgtaaatacctacgggaggcagcagtatgggaataaccctg
Kukkaseq     (  720) -----------------------------------------------------------...................c.......c.t.a....
Ds4seq       (  674) ----------------a.---------------------------------------.................a.............
2301SEQ      (  673) -----------------------------------------------------------..............c............
390seq       (  675) ---------g.g.c...a..t.aa.aataaggaaaaa.......a.........tttc----.gaa........ttc....tg..t..t..t...c..g..cgt.ta.ac.c..c.
H. felis com (  735) -----------------a..t....taag-----------aa..........a-----..a........ttc....tg..t..t..t..c....a.a..g..c.
H. pylori co ( 3352) ---------------a..a.---------a.gga------------ag.ccg.tgaa...a--........ttctctcg.a---.....ttc....tg..t.......t.cg
H. heilmanni (  907) .................a....a.........

Cslseq       (  968) taccgatcttcttggggcaagaagtagaacatgactatataccctatggccgaagaacttaaatttggcgcgggtgaaactatccgtgaggggtatgggtcagagcaataggcgctgataagtgcgcttaggaga
Kukkaseq     (  810) .t.......................................................c......................................g................t..a......
Ds4seq       (  764) ...........................................................t.......g.....................t...................g.........a....
2301SEQ      (  763) .t........................................................c......................................g......g.........a....
390seq       (  765) c..t..t.gatctt..............g..g.....t.gc....t..............g.gc.......g.........a.c........g..cgt..ta.ac.c..c......agctctt.tga
H. felis com (  840) .a..ct.gatc..t......................c............tt........c.......g.gc........g..cc.aa.a..a..c.....atct..c.a....agca..g.aga
H. pylori co ( 3453) .c..t..c..gatcct.....................c.....................gc......t.......a.c......t....g.......c...t.g......a.c.....c....cagcagcc.tga
H. heilmanni ( 1004) .c..t..c..gatcct...........................................c.........................................t..a.........

Cslseq       ( 1088) cctagattagtcatcactaacgcgatgattatcgactacaccggattgggattaaaaagccgacactgggaggcaaaaatccatggcgattggcgcaaggcaggaaacaaggacatgca
Kukkaseq     (  930) .t.............................g..................t..................c.........t..................g..a......
Ds4seq       (  884) .t.................................c..............................t..............t....g..g.....a.....
2301SEQ      (  883) .t.............g...................c.............................t...............g..g...c.t.....a.....
390seq       (  885) .t........................g......t..............g......g...................g.gc.......t..a.gc..t.....a.......
H. felis com (  960) .at..............g.gc.................c..............................t.....g.t...........t..a.gc..t.....a....c.a.......
H. pylori co ( 3573) .gt.g..........a.t............cc.c..g.g..t.g.t...........c.....................g.t..............c..g........c..
H. heilmanni ( 1124) .g..c.....c.t...................c.......................g.g.......................c.g........g............a.......

Cslseq       ( 1208) agatggcgtaagcccctcatatggtcgtggggtgtggcacactgagaagcaaggtatgattattaccgctggggatcgattccacacaccactccttcctttctccacaacaatt
Kukkaseq     ( 1050) ..........................................................................................g..................c.......
Ds4seq       ( 1004) ..........................................................................g............g....................c.......
2301SEQ      ( 1003) ........t.............................................................g...............g..g.........t........c.....c.
390seq       ( 1005) .........gataa.a..c.ttg...a...cct.ct....g...ct.....t....g.a..............t...c.....a.g..t.tt........ta.c........a.
H. felis com ( 1080) ........t.aaaaca..c.tag...a..cct.ct..t....ct.......c......g.a.g.....t...cg.a..g....t.t.ca.......c........a.
H. pylori co ( 3693) ........g.c.......a.t.......c.............g.t.................g.........c...t..g..............t........a.
H. heilmanni ( 1244) ........tt.aacaggc.ctg....a.acct.ct...a.acct.ct.....ct..........g..............ca.c.......t..............a.
```

Figure 1a (2)

```
Cslseq       ( 1328) cctaccgctctagccaatgcgttacaaccatgtttggaggcggcacaggtcctgtagagtggcacgcgaatgcgactactcactccgggtcaaatggaacttgcaccgatgttgcgcgc
Kukkaseq     ( 1170) ...............................a.........c..c............................c...............c.........................
Ds4seq       ( 1124) .t......................................t.....c..c..........................c.......................................
2301SEQ      ( 1123) ................t.............g..........t....c..c..................................................................
390seq       ( 1125) ......t..t..t..gc.g..a..........a.....a...cg........c.........c...a..g.a..t...c..ca.a....
H. felis com ( 1200) .a...t..t.a.gc.a.......a..t.a.c..........ct........a.g.a.t.g...c.ca.a.
H. pylori co ( 3813) a...t.ct.t.tgc.aa.c..c..g..t.a.c..........cc........aa.agaa...c.c..
H. heilmanni ( 1364) ..t...t.ct.t.tgc.aa.c..g..t.a.c..........c..c.c.....

Cslseq       ( 1448) agcagaagagtattctatgaatgtgggctttttgggcaaaggcaatagctctagcaaaaaacaacttgtagaacaagtgacggggcgcggcgatttggtgttttaaattgcatgaaatgcgggg
Kukkaseq     ( 1290) ....................................a.......................................c..c.............c.....................
Ds4seq       ( 1244) .t.............................................................c..t.............c.....................
2301SEQ      ( 1243) .t....................................c..t............................c.....................
390seq       ( 1245) ...........a................c..g...........a.g....ta.g..ccctct.acgc...a..g..............c.c.
H. felis com ( 1320) .c.........a..cg.c.......c.a......ct.g...g....t..cgct...a.g.tgcgagct.a.cc..t..a.t...a.t..c..
H. pylori co ( 3933) ...c..t..ttc......t.a...t..c..tttg..cctgct..ca.t.c.gc.....a.c..
H. heilmanni ( 1484) tt...t......a..cg.c......cc.t..acc.t.g.g...gtg...tttg...cctgct.ca.t.c.gc.....a.c..

Cslseq       ( 1568) cacaacaccaagtcggatcgactgcttagacactgctggtgcagatgaatacgatgtgtcgaagtttgtatccacacgatcaatgaggcaggttatgtgtagatgacacccctaaatgcaat
Kukkaseq     ( 1410) .......t....................a.....................................g................c..c.............g.......g..
Ds4seq       ( 1364) .......t.....................a.........................................g................c..c.............g..
2301SEQ      ( 1363) ...........................a.....................c..t.....................................................
390seq       ( 1365) ...........................c.c.at.c..c....................ggc.....cc.t.c...g..c.g....a........g.g..g.
H. felis com ( 1440) a.gc........t.tc.c........c.c.at.c..c..........cgc.......a.c.tt.g...a.c......ta.ggc..t.
H. pylori co ( 4053) ...c..t..ttc......t.g.ca...ggcg.......a.c..tt.g...a.c..c.g...g..a.........g.a..c.
H. heilmanni ( 1604) ..gc.........ctca..c.....a.c.........gctc.a.a.c..t.ca

Cslseq       ( 1688) gaacgggcgcgccatccacattgaggggaggacactcaactgtgttatccaccatggcaggcgcgagctcaatattctaccctctcctccacaccccactattcc
Kukkaseq     ( 1530) ...........................................a............................................t...........c..
Ds4seq       ( 1484) .................................................a..................................................g..c..
2301SEQ      ( 1483) .......................................c................................................................c..
390seq       ( 1485) ........a....t...c..a.g..t..g.t...a......aa.......g..at.t..c........g....t..t.a..g..c..
H. felis com ( 1560) .a.......a....t.g.ca.t.t....a.c.t.c...g.t.aag.a..c.t.a.a...g....t..g.t..t..t..a..c.c..
H. pylori co ( 4173) tgct..a...a.t.g..ca.t.t...t.c...g.t...c..c.g...aa..g..at.t..c...t..tg.t.t...a..c.c..
H. heilmanni ( 1724) cgct..a...a............ca..t...............c..a..g..........g....a.......c.c..

Cslseq       ( 1808) ctatacacattaatacggttgcagaacatgctcaccacctagacatgggggttgcagcgaagtgatggctcaatttttcctcaaagccgtatccgcgcctctatcgc
Kukkaseq     ( 1650) .........................a.................t...........................c..c.g......................a..........c..
Ds4seq       ( 1604) ..........................t...............c..c.g....................................t..
2301SEQ      ( 1603) ...................c.....................c..c.g..........................................c..
390seq       ( 1605) ...g..............c...c.......t.g..t.a..t..aag.a...g..g..g..cg..ttcga.g..t.......caa..
H. felis com ( 1680) t..c..aa..c..t.aa..c.g..a.g....t.g...gtg.......t.g...g..g..cg.g..ttcaa.g....tcaaa.c..t..
H. pylori co ( 4293) t..c...g.g....a.g......t......t.g..t..aa...aa..a......g.cg..ctca...caaa.c..t..
H. heilmanni ( 1844) t..tc......aa..c..a.aa..c....a.g........t..aaa..a.........g...........a..........a..c..

Cslseq       ( 1928) ggctgaagatgtgctccatgatatggtgtgatcgcgatccgaagcgaagtcgatggctgcgactgcgaagaataaaa
Kukkaseq     ( 1770) c.........................................t...c..c.g.........................a....a..c..
Ds4seq       ( 1724) c.....................................t.c............c..g..........a..........a..
2301SEQ      ( 1723) c......................................t.c........a...................t.c.......a..
390seq       ( 1725) c..........g...........t.c..g...........g....g.....a..a..a..a..c..
H. felis com ( 1800) ........ccaa.....c..........ga.ct.tt.t...c..g.....t..ca.a.......a.t..c..c.c.g..
H. pylori co ( 4413) .........cactt.g...........ga.tt.t.a.c..c..t..t..ca.a............a..c.a..c..
H. heilmanni ( 1961) ....g...........aaa.........c....ga.tt.t.c..c..t......c..t...........a..c.a..c..
```

Figure 1a (3)

Figure 1a (4)

ALIGNED SEQUENCES

Reference molecule: urexCS1   1 -   226   (226 aa)   Homology

Sequence 2: urexXkuka   1 -   226   (226 aa)   100%
Sequence 3: urexDS4   1 -   226   (226 aa)   99%
Sequence 4: urex2301   1 -   226   (226 aa)   99%
Sequence 5: urex390   1 -   226   (226 aa)   99%
Sequence 6: A felis   1 -   237   (237 aa)   50%
Sequence 7: A pylori   1 -   238   (238 aa)   52%
Sequence 8: A heilman   1 -   234   (234 aa)   54%

Alignment type: Global Protein
Parameters: Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N

urexCS1   1) vkltpkeqekrllyyagevarkrkaeglklnqpealayisahindearrgkktvaqlmeecmhflkkdevmpgvgnmvpdlgveatfpdgtklvtvnwpiepdehfkagevkfgcdkdie
urexXkuka   1) ....e...........................
urexDS4   1) ....e...........................
urex2301   1) ?...e...........................
urex390   1) ....e...........................
A felis   1) m.......ld.lm.h....rl.eeal.r.v....yt.v.l..grv.ek.d.n.s..d..q.grtw...en..d..as.ihev.i..n........iht.v.dngklap...-l.kne..t
A pylori   1) m.......ld.lm.h....l.k..ek.i...yt.v.l...e..a...a.e..q.grtl..p.d..d..as.ihev.i..m.........ht..angklvp.-l.kne..t
A heilman   1) m.......ld.lm.h....l.kq...k.l...yt.v.l...v.e..a...s..d..q.grtl..a.d.....ah.ihev.i..g..........iht.v.agsdkl.pgevilkne.t

urexCS1   121) lnagkevtelevtnegpkslhvgshfhffeankalkfdrekaygkrldipsgntlrigagqtrkvqliplggskkvigmnglvnniaderhkhkaldkakshgfi------------k
urexXkuka   121) ....
urexDS4   121) ....
urex2301   121) ....e...........
urex390   121) ....t..
A felis   120) i..v..ais.k.k.drpvq.........v.l.d....a.sfc....a.tav.fep.eeks.e..di..riy.f.s..drq..adg.klg.kr..ek..gsvncgceatkdk-q
A pylori   120) i.e.kavsvk.v.drpvqi.......v.rc.d......tf.......a.tav.fep.eeks.e..di..nrrif.f.a..drq..nes.ki.hr..er..hgaksddnyvktike
A heilman   121) .....havq.k.k.drpvq.........v.l.d.........a.tav.fep.eekt.e..di..n.riy.f.a..drq..hdg.kl.kr..ekh.gtincgcdn----.

Figure 1b

ALIGNED SEQUENCES

Reference molecule: ureYCS1

		1 -	568	(568 aa)	Homology

Sequence 2: ureYkuka   1 - 568 (568 aa) 99%
Sequence 3: ureYDS4   1 - 568 (568 aa) 98%
Sequence 4: ureY2301   1 - 568 (568 aa) 99%
Sequence 5: ureY390   1 - 496 (496 aa) 86%
Sequence 6: B felis   1 - 569 (569 aa) 73%
Sequence 7: B pylori   1 - 569 (569 aa) 73%
Sequence 8: B heilman   1 - 568 (568 aa) 74%

Alignment type: Global Protein
Parameters: Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N

```
ureYCS1   1) mkmkkq-eyvntygptkgdkvrlgdtdlwaevehdytygeelkfgagktiregmgqsnspdentldlvitnamiidytgiykadigiknqkihgigkagnkdmgdgvsphmvvgvgtea
ureYkuka  1) ...................t...............................................................................................
ureYDS4   1) ...................t...............................................................................................
ureY2301  1) ...................t...............................................................................................
ureY390   1) ...................t...............................................................................................
B felis   1) ...kisrk....sm.....t.r.............il.......g...d.s.t..ssye....l...l.v..............d........dnnlc.pa...............
B pylori  1) ...kisrk....sm.....t...............il.......g...d.s.t..ssye.i...l.v..............d..a....g.....knnls.pa...........
B heilman 1) ...kisrk....sm.....t...............il.......g...d...t..sshe.......l.v........................cnrlc.pa...........

ureYCS1   120) lagegmiitaggidshthflspqqfptalangvttmfgggtgppvdgtnattitpgkwnlhrmlraaeeysmnvgflgkgnsssskkqlveqveagaigfklhedwgttpsaidhclsvade
ureYkuka  120) ..............................................................................................................................
ureYDS4   120) ..............................................................................................................................
ureY2301  120) ..............................................................................................................................
ureY390   120) .a..l..........t.i.l...l...f.s......a.........ra..ks........a..l..a..v.yeps.rd.i......i.......s..a..h..n..........
B felis   121) .a..l.v........t.i.l...i...f.s.........a.........rr..kw........l..a..a.ndas.ad.i......i.......s..n.a.d..k..........
B pylori  121) .a..l.v........t.i.l...i...f.si.l.....a...........r..ke........s..a..l.y....v.fepa.id.l.......s......n.a.ni..k..........
B heilman 121) .a..l.v........t.i.l...i...f.s.i......a...........r..ke........s..a..l.y....v.fepa.id.l.......s......n.a.ni..k.

ureYCS1   240) ydvqvcihtdtvneagyvddtlnamngraihayhiegagghspdvitmagelnilpssttptipytintvaehldmlmtchhidkrireдlqfsqsrirppgsiaaedvlhdmgviants
ureYkuka  240) ...........................................v................................................i.............
ureYDS4   240) ...........................................................................................i...............
ureY2301  240) ......l....c.e.e.ia..t.tf.t....a....k....f....a.n....f.k..e....m....v.........s.k.v..ad........qt...q.....ifsi.
ureY390   240) ......l....c.e.e.ia..t.tf.t....a....k....f....a.n....f.v..e....m....v.........s.k.v..ad........qt....t....ifsi.
B felis   241) ......a....l....c.e..ma.ia..tm.tf.t....a.i.kv..h....a.n....f...a.n.........n.k.ve.ad........qt....k.....ifsi.
B pylori  241) ......a....l....c.e..e.ia..t.tf.t....a....k....f....a.n....f.k..e....m.......n.k.ve.ad........qt....k.....ifsi.
B heilman 241) ......a....l....c.e..e.ia..t.tf.tf....sa................a.......................................i.

ureYCS1   360) sdsqamgrageviprtwqtadknkkefgklpedgkdndnfrikryiskytinpalthgvseyigsveegkiadlvvwnpaffgvkpkivikggmvvfsemgdsnasvptpqpvyyremfg
ureYkuka  360) ................................................sa....a.................................................
ureYDS4   360) ...............................................a......a...............................................
ureY2301  360) .......................a......a.................................................................a
ureY390   360) .......t...........a......gia..i.d.v...v..y....l.s......i...nmi....fial.q....a..i.................a
B felis   361) .......v...t.........r.k.ekg........ia.i..v....l.s......i...nmi....fial.q....a..i.....................
B pylori  361) .......v...t.........r.k.ekg..........i..v....l.s......i...nmi....fial.q....a..i.....................
B heilman 361) .......v...t.........r...ekg..........i..v..y....l.s......i...nmi....fial.q....a..i.....................
```

```
ureYCS1   480) hhgkakfdtsitfvskvayengvkeklglerqvlpvkncrnitkkdfkfndktakitvdpktfevfvdgklctskptsqvplaqrytff
ureYkuka  480) .........................................k....................................e..............
ureYDS4   480) .........................................k.......n....h..................a.e.................
urey2301  480) .........................................k.......n....h.............................rvss.....
urey390   480) ............................------------------..........l....v.h.d.n.e.yk.k.....ev...aadels...l.nl.
B felis   481) ...n...n.........qa..ka.i..e...d.aap..........l....v.h.d.n.e.yk.k.....ev...ank.s...lfsi.
B pylori  481) ...y.an......qa..dk.i..e................mq..t..h.e.n.e.yh......ev...ank.s...lfsi.
B heilman 480) .........q.......i.he...q.v............l....v..h.e.n.e.yk.k....nev..haadkls...l.nl.
```
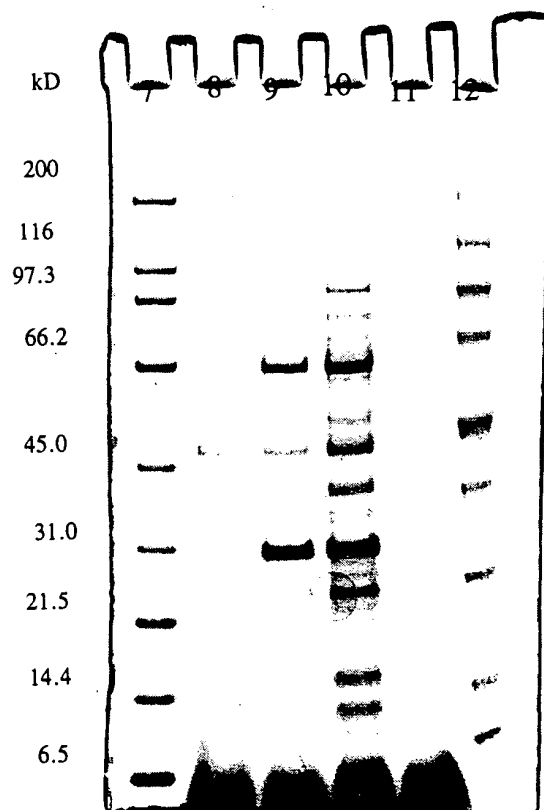
Figure 1c (2)

Figure 2